SEQUENCE LISTING

<110> Sprecher, Cindy A.
Kisiel, Walter
Foster, Donald C.

<120> NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND METHODS RELATING THERETO

<130> 93-14D4

<150> US 09/904,621
<151> 2001-07-13

<150> US 09/265,627
<151> 1999-03-09

<150> US 08/457,887
<151> 1995-06-01

<150> US 08/147,710
<151> 1993-11-05

<160> 15

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                                          Met Asp Pro Ala Arg Pro
                                           1               5

ctg ggg ctg tcg att ctg ctg ctt ttc ctg acg gag gct gca ctg ggc   104
Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly
            10                  15                  20

gat gct gct cag gag cca aca gga aat aac gcg gag atc tgt ctc ctg   152
Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu
        25                  30                  35

ccc cta gac tac gga ccc tgc cgg gcc cta ctt ctc cgt tac tac tac   200
Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr
    40                  45                  50

gac agg tac acg cag agc tgc cgc cag ttc ctg tac ggg ggc tgc gag   248
Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu
55                  60                  65                  70

ggc aac gcc aac aat ttc tac acc tgg gag gct tgc gac gat gct tgc   296
Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys
                75                  80                  85
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tgg agg ata gaa aaa gtt ccc aaa gtt tgc cgg ctg caa gtg agt gtg   344
Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val
            90                  95                 100

gac gac cag tgt gag ggg tcc aca gaa aag tat ttc ttt aat cta agt   392
Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser
        105                 110                 115

tcc atg aca tgt gaa aaa ttc ttt tcc ggt ggg tgt cac cgg aac cgg   440
Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg
    120                 125                 130

att gag aac agg ttt cca gat gaa gct act tgt atg ggc ttc tgc gca   488
Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala
135                 140                 145                 150

cca aag aaa att cca tca ttt tgc tac agt cca aaa gat gag gga ctg   536
Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu
                155                 160                 165

tgc tct gcc aat gtg act cgc tat tat ttt aat cca aga tac aga acc   584
Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr
            170                 175                 180

tgt gat gct ttc acc tat act ggc tgt gga ggg aat gac aat aac ttt   632
Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn Phe
        185                 190                 195

gtt agc agg gag gat tgc aaa cgt gca tgt gca aaa gct ttg aaa aag   680
Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys
    200                 205                 210

aaa aag aag atg cca aag ctt cgc ttt gcc agt aga atc cgg aaa att   728
Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile
215                 220                 225                 230

cgg aag aag caa ttt taa acattcttaa tatgtcatct tgtttgtctt          776
Arg Lys Lys Gln Phe  *
                235

tatggcttat ttgcctttat ggttgtatct gaagaataat atgacagcat gaggaaacaa 836
atcattggtg atttattcac cagtttttat taatacaagt cacttttttca aaaatttgga 896
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caactgtttg tgagactgaa ttc                                         979
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Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
            20                  25                  30
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
        35                  40                  45
Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
    50                  55                  60
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
65                  70                  75                  80
Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys
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                85                  90                  95
Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys
            100                 105                 110
Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly
        115                 120                 125
Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr
    130                 135                 140
Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser
145                 150                 155                 160
Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe
                165                 170                 175
Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly
            180                 185                 190
Gly Asn Asp Asn Asn Phe Val Ser Arg Glu Asp Cys Lys Arg Ala Cys
        195                 200                 205
Ala Lys Ala Leu Lys Lys Lys Lys Lys Met Pro Lys Leu Arg Phe Ala
    210                 215                 220
Ser Arg Ile Arg Lys Ile Arg Lys Lys Gln Phe
225                 230                 235
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<222> (77)...(235)

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ataaacgacc aaaaga atg aag gct gtt ttc ttg gtt ttg tcc ttg atc gga 112
Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly
1 5 10

ttc tgc tgg gcc caa cca gtc act ggc gat gaa tca tct gtt gag att 160
Phe Cys Trp Ala Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile
15 20 25

ccg gaa gag tct ctg atc atc gct gaa aac acc act ttg gct aac gtc 208
Pro Glu Glu Ser Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val
30 35 40

gcc atg gct gag aga ttg gag aag aga 235
Ala Met Ala Glu Arg Leu Glu Lys Arg
45 50

<210> 8
<211> 53
<212> PRT
<213> Homo sapiens

<400> 8
Met Lys Ala Val Phe Leu Val Leu Ser Leu Ile Gly Phe Cys Trp Ala
1 5 10 15
Gln Pro Val Thr Gly Asp Glu Ser Ser Val Glu Ile Pro Glu Glu Ser
20 25 30
Leu Ile Ile Ala Glu Asn Thr Thr Leu Ala Asn Val Ala Met Ala Glu
35 40 45
Arg Leu Glu Lys Arg
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<210> 9
<211> 17
<212> DNA
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<220>
<223> Nor-1478

<400> 9
gtaaaacgac ggccagt 17

<210> 10
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<220>
<223> NOR-2523

<400> 10
tctcttctcc aatctctcag c 21

<210> 11
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<212> DNA
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<220>
<223> M-2162

<400> 11
cttttactct agacttactt tggtgcgcag aagcc 35

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal

<400> 12
Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
1 5 10

<210> 13
<211> 8
<212> PRT
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<400> 13
Ala Gln Glu Pro Thr Gly Asn Asn
1 5

<210> 14
<211> 165
<212> DNA
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<221> variation
<222> (0)...(0)
<223> Kunitz domain

<221> variation
<222> (1)...(3)
<223> Codon-1 Wherein the nucleotide triplet 1-3
encodes any amino acid except cysteine.

<221> variation
<222> (4)...(6)
<223> Codon-2 Wherein the nucleotide triplet 4-6

encodes any amino acid except cysteine.

<221> variation
<222> (160)...(162)
<223> Codon-54 Wherein the nucleotide triplet 160-162 encodes any amino acid except cysteine.

<221> variation
<222> (163)...(165)
<223> Codon-55 Wherein the nucleotide triplet 163-165 encodes any amino acid except cysteine.

<400> 14
nnnnnntgtc tcctgcccct agactacgga ccctgccggg ccctacttct ccgttactac 60
tacgacaggt acacgcagag ctgccgccag ttcctgtacg ggggctgcga gggcaacgcc 120
aacaatttct acacctggga ggcttgcgac gatgcttgcn nnnnn 165

<210> 15
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Kunitz Domain

<221> VARIANT
<222> (1)...(2)
<223> aa1-2 Wherein each amino acid from position 1 to 2 is individually any amino acid except cysteine.

<221> VARIANT
<222> (54)...(55)
<223> aa54-55 Wherein each amino acid from position 54 to 55 is individually any amino acid except cysteine.

<400> 15
Xaa Xaa Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu
1 5 10 15
Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu
20 25 30
Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala
35 40 45
Cys Asp Asp Ala Cys Xaa Xaa
50 55